

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:47:41 ; Search time 30.9604 Seconds  
(without alignments)  
711.279 Million cell updates/sec

Title: US-10-009-431-3

Perfect score: 1550

Sequence: 1 MLVLVLVSLWPLPGGALSIA.....DTGVSLQTYDDLLAKDCHCI 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/protdata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/protdata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/protdata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/protdata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/protdata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/protdata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1550	100.0	308	3	US-08-775-882-4
2	1550	100.0	308	3	US-08-775-882-6
3	1550	100.0	308	4	US-09-276-600-6
4	1550	100.0	308	4	US-09-976-594-449
5	1550	100.0	308	4	US-09-919-039-192
6	1546	99.7	308	3	US-09-927-433-9
7	1546	99.7	314	4	US-09-949-016-10118
8	1542	99.5	295	2	US-08-411-607A-2
9	1542	99.5	295	4	US-09-361-741-2
10	1542	99.5	295	4	US-09-461-418-2
11	1531	98.8	308	4	US-09-949-016-6559
12	659	42.5	119	4	US-08-626-185-4
13	624	40.3	112	3	US-08-927-433-8
14	624	40.3	112	3	US-08-927-433-10
15	545	35.2	99	3	US-08-775-882-2
16	460	29.7	115	4	US-09-463-931-2
17	229	14.8	513	2	US-08-459-346-19
18	229	14.8	513	2	US-07-989-847-8
19	229	14.8	513	3	US-08-889-419-19
20	229	14.8	513	3	US-08-469-411-8
21	229	14.8	513	3	US-08-402-542-19
22	229	14.8	513	4	US-09-780-601A-8
23	229	14.8	513	4	US-09-949-016-6118
24	229	14.8	513	5	PCT-US93-07189-19
25	229	14.8	513	6	5187076-6
26	229	14.8	513	6	5187076-6
27	229	14.8	563	4	US-09-949-016-11259

28	221	14.3	372	1	US-08-278-729A-33	Sequence 33, Appl
29	221	14.3	372	1	US-08-155-343A-33	Sequence 33, Appl
30	221	14.3	372	1	US-08-406-672-33	Sequence 33, Appl
31	221	14.3	372	1	US-08-643-563A-33	Sequence 33, Appl
32	221	14.3	372	1	US-08-643-763A-33	Sequence 33, Appl
33	221	14.3	372	1	US-08-462-623-33	Sequence 33, Appl
34	221	14.3	372	1	US-08-451-953A-33	Sequence 33, Appl
35	221	14.3	372	2	US-08-459-346-15	Sequence 15, Appl
36	221	14.3	372	2	US-08-445-468A-33	Sequence 33, Appl
37	221	14.3	372	2	US-08-461-397A-33	Sequence 33, Appl
38	221	14.3	372	2	US-08-912-088-33	Sequence 33, Appl
39	221	14.3	372	3	US-08-278-730A-33	Sequence 33, Appl
40	221	14.3	372	3	US-08-889-419-15	Sequence 15, Appl
41	221	14.3	372	3	US-08-445-467-33	Sequence 33, Appl
42	221	14.3	372	3	US-08-480-515A-33	Sequence 33, Appl
43	221	14.3	372	3	US-09-170-936-33	Sequence 33, Appl
44	221	14.3	372	3	US-08-402-542-15	Sequence 15, Appl
45	221	14.3	372	3	US-08-461-113-33	Sequence 33, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-775-882-4

/ Sequence 4, Application US/08775882

/ Patent No. 6180602

/ GENERAL INFORMATION:

/ APPLICANT: KATO, Seishi

/ APPLICANT: OH, Suwan

/ APPLICANT: SEKINE, Shingo

/ APPLICANT: SAEKI, Mihoro

/ APPLICANT: KOBAYASHI, Midori

/ APPLICANT: YADA, Mika

/ APPLICANT: TSUJI, Tomoko

/ APPLICANT: OHMORI, Hitoshi

/ TITLE OF INVENTION: HUMAN NOVEL CDNA, TGF-BETA SUPERFAMILY

/ TITLE OF INVENTION: PROTEIN ENCODED THEREBY AND THE USE AS IMMUNOSUPPRESSIVE

/ NUMBER OF SEQUENCES: 10

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Foley & Lardner

/ STREET: 3000 K Street, N.W., Suite 500

/ CITY: Washington

/ STATE: D.C.

/ COUNTRY: USA

/ ZIP: 20007-5109

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/775,882

/ FILING DATE: 02-JAN-1997

/ CLASSIFICATION: S14

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/390,207

/ FILING DATE: 16-FEB-1995

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/379,441

/ FILING DATE: 03-FEB-1995

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: JP 5-61431

/ FILING DATE: 26-FEB-1993

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: JP 4-327619

/ FILING DATE: 13-NOV-1992

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: JP 4-208077

/ FILING DATE: 04-AUG-1992

/ ATTORNEY/AGENT INFORMATION:

/ NAME: WEGNER, Harold C.

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:49:12 ; Search time 85.2871 Seconds  
(without alignments)  
1245.908 Million cell updates/sec

Title: US-10-009-431-3

Perfect score: 1550

Sequence: 1 MLLVLLVLSWLPHGALSLA.....DTGVSLQTYDDLLAKDCHCI 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap:\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1550	100.0	308	9	US-09-276-600-6
2	1550	100.0	308	9	US-09-276-600-6
3	1550	100.0	308	10	US-09-981-353-188
4	1550	100.0	308	13	US-09-919-039-192
5	1550	100.0	308	15	US-10-000-628-6
6	1546	99.7	308	16	US-10-257-597-2
7	1542	99.5	295	9	US-10-425-115-229584
8	1542	99.5	308	15	US-09-361-741-2
9	1538	99.2	295	14	US-10-211-689-72
10	1537	99.2	308	15	US-10-270-377-2
11	1531	98.8	308	15	US-10-257-597-1
12	1531	98.8	308	14	US-10-205-823-327
					Sequence 113, App

13	1531	98.8	308	15	US-10-295-027-618	Sequence 618, App
14	1531	98.8	308	15	US-10-295-027-618	Sequence 1379, App
15	1531	98.8	308	15	US-10-211-462-191	Sequence 191, App
16	1531	98.8	308	16	US-10-448-664-2	Sequence 2, Appli
17	1464	94.5	283	15	US-10-211-689-76	Sequence 76, Appli
18	884.5	57.1	298	9	US-09-789-919-68	Sequence 68, Appli
19	659	42.5	119	15	US-10-373-581-4	Sequence 4, Appli
20	540	34.8	102	15	US-10-211-689-74	Sequence 74, Appli
21	460	22.7	115	14	US-10-194-382-2	Sequence 2, Appli
22	244	15.7	45	16	US-10-408-765A-976	Sequence 976, App
23	229	14.8	513	14	US-10-122-026-19	Sequence 19, Appli
24	229	14.8	513	14	US-10-164-279-33	Sequence 33, Appli
25	229	14.8	513	15	US-10-366-345-38	Sequence 38, Appli
26	229	14.8	513	15	US-10-291-265-816	Sequence 816, App
27	229	14.8	513	15	US-10-375-150-8	Sequence 8, Appli
28	221	14.3	372	8	US-08-260-675-33	Sequence 33, Appli
29	221	14.3	372	10	US-09-952-318A-33	Sequence 33, Appli
30	221	14.3	372	14	US-10-122-026-15	Sequence 15, Appli
31	221	14.3	372	14	US-10-050-050-33	Sequence 33, Appli
32	221	14.3	372	14	US-10-164-279-49	Sequence 49, Appli
33	221	14.3	372	15	US-10-366-345-49	Sequence 49, Appli
34	221	14.3	372	15	US-10-295-027-244	Sequence 244, App
35	221	14.3	373	9	US-09-813-398-36	Sequence 36, Appli
36	221	14.3	373	16	US-10-826-324-36	Sequence 36, Appli
37	219.5	14.2	438	14	US-10-122-026-14	Sequence 14, Appli
38	218	14.1	437	9	US-09-784-911-4	Sequence 4, Appli
39	214.5	13.8	347	14	US-10-274-971-2	Sequence 2, Appli
40	212.5	13.7	281	15	US-10-375-150-12	Sequence 12, Appli
41	212.5	13.7	402	10	US-09-952-318A-21	Sequence 21, Appli
42	212.5	13.7	402	14	US-10-050-050-21	Sequence 21, Appli
43	212.5	13.7	402	14	US-10-164-279-45	Sequence 45, Appli
44	212.5	13.7	402	15	US-10-366-345-40	Sequence 40, Appli
45	212.5	13.7	403	9	US-09-813-398-31	Sequence 31, Appli

#### ALIGNMENTS

RESULT 1  
US-09-276-600-6  
; Sequence 6, Application US/09276600  
; Patent No. US20010010908A1  
; GENERAL INFORMATION:  
; APPLICANT: Patricia Billing-Medel  
; APPLICANT: Maurice Cohen  
; APPLICANT: Tracey L. Colpitts  
; APPLICANT: Julian Gordon  
; APPLICANT: Edward N. Granados  
; APPLICANT: John C. Russell  
; APPLICANT: Stephen D. Stroupe  
; TITLE OF INVENTION: Reagents and Methods Useful for  
; TITLE OF INVENTION: Detecting Disease of the Prostate  
; FILE REFERENCE: 6397 US 01  
; CURRENT APPLICATION NUMBER: US/09/276,600  
; CURRENT FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-276-600-6

Query Match 100.0%; Score 1550; DB 9; Length 308;  
Best Local Similarity 100.0%; Pred. No. 2.2e-120; Indels 0; Gaps 0;  
Matches 295; Conservative 0; Mismatches 0;  
Qy 1 MLLVLLVLSWLPHGALSLAASPPGSELTEDSRFELKRYEDLLTRANQSW 60  
Db 14 MLLVLLVLSWLPHGALSLAASPPGSELTEDSRFELKRYEDLLTRANQSW 73  
Qy 61 EDSDNDLVAPAVRILPPEVRLGSGGHLHRIISRAALPEGLPEASRLHRLFRISPTASR 120

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:10 ; Search time 89.9604 Seconds  
(without alignments)  
1679.221 Million cell updates/sec

Title: US-10-009-431-3

Perfect score: 1550

Sequence: 1 MLVLVLVSLWPHGGLSLA.....DTGNSLQTYDDLLAKDCHCI 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1550	100.0	308	1	GDFP_HUMAN
2	1546	99.7	308	2	Q9BWA0
3	911.5	58.8	303	1	GDFP_MOUSE
4	909.5	58.7	303	2	Q6NX53
5	887.5	57.3	303	1	GDFP_RAT
6	255.5	16.5	387	2	Q869H8
7	240.5	15.5	373	2	Q98950
8	237.5	15.3	373	2	Q90723
9	230	14.8	350	2	Q645R0
10	229	14.8	513	1	BMP6_HUMAN
11	221	14.3	372	1	GDF1_HUMAN
12	220	14.2	506	2	Q811S4
13	218	14.1	461	1	GDF7_MOUSE
14	216	13.9	301	2	Q86RL7
15	216	13.9	435	2	Q8BRW3
16	216	13.9	510	1	BMP6_MOUSE
17	215.5	13.9	365	2	Q765I4
18	215	13.9	424	2	Q6P4J4
19	214.5	13.8	347	1	NODA_HUMAN
20	214.5	13.8	365	2	Q02424
21	212.5	13.7	402	1	BMBB_HUMAN
22	212.5	13.7	402	2	Q725V6
23	212	13.7	354	1	NODA_MOUSE
24	211.5	13.6	453	2	Q75RY1
25	210.5	13.6	453	1	GDF9_CAPHI
26	210	13.5	350	2	Q66KL4
27	210	13.5	354	2	Q8BH87
28	209.5	13.5	294	2	Q9BDW9
29	209.5	13.5	447	1	GDF7_CERAE
30	208.5	13.5	289	2	Q9XYQ8
31	208.5	13.5	450	1	GPDT_HUMAN

32	208	13.4	207	1	BMP6_RAT	Q04906	rattus norv
33	208	13.4	417	2	Q9XIQ7	Q9XYQ7	lytechinus
34	208	13.4	430	1	BMP7_MOUSE	P23359	mus musculus
35	207.5	13.4	453	1	GDF9_SHEEP	O77681	ovis aries
36	207	13.4	431	1	BMP7_HUMAN	P18075	homo sapien
37	207	13.4	441	2	Q6PUD1	O6pud1	anopheles g
38	207	13.4	441	2	Q7PZ17	Q7pzi7	anopheles g
39	207	13.4	452	2	Q6HA10	Q6ha10	rattus norv
40	206.5	13.3	454	1	BMP5_HUMAN	P22003	homo sapien
41	205.5	13.3	361	2	Q96504	Q96504	branchiost
42	205.5	13.3	424	2	Q9YGH7	Q9ygh7	xenopus lae
43	205.5	13.3	446	2	Q7T288	Q7t288	brachydanio
44	205	13.2	452	1	BMP5_MOUSE	P49003	mus musculus
45	205	13.2	454	2	Q8CCB0	Q8cce0	mus musculus

#### ALIGNMENTS

RESULT 1  
ID GDFP\_HUMAN STANDARD; PRT; 308 AA.  
AC Q99988; O14629; P78360; Q9NRT0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 44, Last sequence update)  
DE Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1).  
DE Name=GDF15; Synonyms=MIC1, PDF, PLAB, PTGFB;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibroarcoma;  
RX MEDLINE=98006316; PubMed=9348093;  
RA Yokoyama-Kobayashi M., Saeki M., Sekine S., Kato S.;  
RT "Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in placenta";  
RL J. Biochem. 122:622-626(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=97470998; PubMed=9326641; DOI=10.1073/pnas.94.21.11514;  
RX Bootcov M.R., Bauskin A.R., Valenzuela S.M., Moore A.C., Bansal M., He X.Y., Zhang H.P., Donnellan M., Mahler S., Pryor K., Walsh B.J., Nicholson R.C., Fairlie W.D., Por S.B., Robbins J.M., Breit S.N.;  
RT "MIC-1, a novel macrophage inhibitory cytokine, is a divergent member of the TGF-beta superfamily";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:11514-11519(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=98041637; PubMed=9375789; DOI=10.1016/S0167-4781(97)00122-X;  
RA Hromas R., Hufford M., Sutton J., Xu D., Li Y., Lu L.;  
RT "PLAB, a novel placental bone morphogenetic protein";  
RL Biochim. Biophys. Acta 1354:40-44(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=98256302; PubMed=9593718; DOI=10.1074/jbc.273.22.13760;  
RA Paralkar V.M., Vail A.L., Grasser W.A., Brown T.A., Xu H., Vukicevic S., Ke H.Z., Qi H., Owen T.A., Thompson D.D.;  
RT "Cloning and characterization of a novel member of the transforming growth factor-beta/bone morphogenetic protein family";  
RL J. Biol. Chem. 273:13760-13767(1998).  
RN [5]  
RP SEQUENCE OF 14-308 FROM N.A.  
RX MEDLINE=98085971; PubMed=9426002; DOI=10.1016/S0378-1119(97)00485-X;  
RA Lawton L.N., de Fatima Bonaldo M., Jelenc P.C., Qiu L., Baumes S.A., Marcelino R.A., de Jesus G.M., Wellington S., Knowles J.A.,

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:46 ; Search time 25.703 Seconds  
(without alignments)  
1104.306 Million cell updates/sec

Title: US-10-009-431-3  
Perfect score: 1550  
Sequence: 1 MLVLVLSWLPVPGGALSLSA.....DTGVSLQTYDILLAKDCHCI 295

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1522.5	98.2	309	2 J05697	placental transfer
2	229	14.8	513	1 BMH06	bone morphogenetic
3	221	14.3	372	2 C39364	GDF-1 embryonic gr
4	216	13.9	510	2 A54798	Vg-1-related prote
5	215.5	13.9	365	2 T43286	cat-1 protein - Ca
6	212.5	13.7	402	2 A45056	osteogenic protein
7	212	13.7	354	2 S29718	gene nodal protein
8	208	13.4	207	2 S37618	vgr protein - rat
9	207	13.4	431	1 BMH07	bone morphogenetic
10	206.5	13.3	454	1 BMH05	bone morphogenetic
11	205	13.2	452	2 I49542	bone morphogenetic
12	204	13.2	360	2 A29619	Vgl embryonic grow
13	204	13.2	430	2 J01184	osteogenic protein
14	202	13.0	313	2 I51284	bone morphogenetic
15	199	12.8	455	2 A43918	TGF-beta-related p
16	196	12.6	426	2 JH0690	bone morphogenetic
17	193	12.5	350	2 J05241	activin beta E cha
18	189.5	12.2	441	2 S45284	growth/differentia
19	188	12.1	398	2 JH0687	bone morphogenetic
20	187	12.1	357	2 A39364	GDF-1 embryonic gr
21	185.5	12.0	588	2 A26158	decapentaplegic pr
22	183	11.8	398	2 JH0688	bone morphogenetic
23	182.5	11.8	151	2 S43296	bone morphogenetic
24	179	11.5	393	2 S37073	bone morphogenetic
25	177	11.4	436	2 B55452	cartilage-derived
26	176	11.4	408	2 S58791	bone morphogenetic
27	175	11.3	501	2 J02347	growth/differentia
28	174.5	11.3	476	2 J04646	bone morphogenetic
29	174	11.2	461	2 S52408	SPDVR1 protein - s

30	173	11.2	501	2 A55452	cartilage-derived
31	172.5	11.1	408	2 S38343	bone morphogenetic
32	171	11.0	400	2 A49147	bone morphogenetic
33	171	11.0	401	2 JH0689	bone morphogenetic
34	171	11.0	495	2 S43294	bone morphogenetic
35	170	11.0	408	1 BMH04	bone morphogenetic
36	169.5	10.9	420	2 I49541	bone morphogenetic
37	169.5	10.9	478	2 J04838	bone morphogenetic
38	168.5	10.9	366	2 A46607	growth/differentia
39	168	10.8	125	2 S43295	bone morphogenetic
40	167.5	10.8	394	2 S45355	bone morphogenetic
41	167	10.8	390	1 WFH02	transforming growt
42	167	10.8	390	2 A27512	transforming growt
43	166.5	10.7	391	2 S01413	transforming growt
44	166	10.7	352	2 J02466	inhibin beta-C cha
45	165.5	10.7	373	2 A41918	transforming growt

ALIGNMENTS

RESULT 1

JC5697  
placental transforming growth factor-beta homolog - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Nov-1997 #sequence\_revision 20-Nov-1997 #text\_change 09-Jul-2004  
C;Accession: JC5697  
R;Yokoyama-Kobayashi, M.; Saeki, M.; Sekine, S.; Kato, S.  
J. Biochem. 122, 622-626, 1997

A;Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in  
A;Reference number: JC5697; MUID:98006316; PMID:9348093  
A;Accession: JC5697  
A;Molecule type: mRNA  
A;Residues: 1-309 <YOK>

A;Cross-references: UNIPROT:Q9BWA0; DDBJ:AB000584  
A;Experimental source: fibrosarcoma  
C;Comment: This protein plays a role in reproduction.

Query Match 98.2%; Score 1522.5; DB 2; Length 309;  
Best Local Similarity 99.0%; Pred. No. 1.1e-108;  
Matches 293; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	1	MLVLVLSWLPVPGGALSLSAASRASFPGPS-ELHTEDSPRELKKEYEDLLTLRANQS	59
Db	14	MLVLVLSWLPVPGGALSLSAASRASFPGPS-ELHTEDSPRELKKEYEDLLTLRANQS	73
Qy	60	WEDSNTDLVPAPAVRILTPVRLGSGGHLRLSRALPEGLPEASRLHRLPRLSPTAS	119
Db	74	WEDSNTDLVPAPAVRILTPVRLGSGGHLRLSRALPEGLPEASRLHRLPRLSPTAS	133
Qy	120	RSWDVTRPLRRLQSLARPQALHLRLSPPPSQSDQLAESSSARPOLEHLRPAARGR	179
Db	134	RSWDVTRPLRRLQSLARPQALHLRLSPPPSQSDQLAESSSARPOLEHLRPAARGR	193
Qy	180	RRARANGDHCPLGRCRCRLHTVRASLEDLGHADWVLSPREVQVTWCIGACPSQFAAN	239
Db	194	RRARANGDHCPLGRCRCRLHTVRASLEDLGHADWVLSPREVQVTWCIGACPSQFAAN	253
Qy	240	MHAQIKTSLHRLKPDTPVAPCCVPASYNPMVLQKTDGTGVSLOTYYDILLAKDCHCI	295
Db	254	MHAQIKTSLHRLKPDTPVAPCCVPASYNPMVLQKTDGTGVSLOTYYDILLAKDCHCI	309

RESULT 2

BMH06  
bone morphogenetic protein 6 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 18-Oct-1991 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: B39263  
R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Wang, E.A.; Woz

Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990  
A;Title: Identification of transforming growth factor beta family members present in bo  
A;Reference number: A39263; MUID:91088608; PMID:2263636

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:44:20 ; Search time 99.8911 Seconds  
(without alignments)  
1142.187 Million cell updates/sec

Title: US-10-009-431-3

Perfect score: 1550

Sequence: 1 MLVLVLSWLPHGGLSLA.....DTGVSLQTVDDLLAKDCHCI 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1550	100.0	295	4	AAB36557 Human GDF
2	1550	100.0	308	2	AAR77097 Human TGF
3	1550	100.0	308	2	AAW10662 Human TGF
4	1550	100.0	308	3	AAB26122 Human TGF
5	1550	100.0	308	5	ABE09174 Human TGF
6	1550	100.0	308	5	ABE09174 Human TGF
7	1550	100.0	308	6	AAE13538 Human mac
8	1550	100.0	308	6	ADAL1070 Human CDN
9	1550	100.0	308	8	ADG77027 Human pro
10	1546	99.7	308	8	ADL12720 Human ste
11	1546	99.7	308	2	AAR84710 Human emb
12	1546	99.7	308	2	AAW10673 Human TGF
13	1546	99.7	308	2	AAW10666 Human TGF
14	1546	99.7	308	2	AAW10672 Human TGF
15	1546	99.7	308	2	AAW10668 Human TGF
16	1546	99.7	308	2	AAW10667 Human TGF
17	1546	99.7	308	2	AAW10671 Human TGF
18	1546	99.7	308	2	AAW48672 Human TGF
19	1546	99.7	308	7	ADI63071 Human apo
20	1542	99.5	308	8	ABM82070 Tumour-as
21	1542	99.5	308	8	ADG71946 Human NOV
22	1538	99.2	295	2	ADJ87283 Human G p
23	1537	99.2	308	2	AAW02613 Human pro
24	1537	99.2	308	2	AAW10670 Human TGF
25	1537	99.2	308	2	AAW10669 Human TGF
					AAE13539 Human mac

26	1535	99.0	318	2	AAW10663	Aaw10663 Human TGF
27	1531	98.8	308	6	ABU03550	Abu03550 Angiogene
28	1531	98.8	308	6	ABU56743	Abu56743 Lung canc
29	1531	98.8	308	7	ADB75503	ADB75503 Prostate
30	1531	98.8	308	7	ADN39300	Adn39300 Cancer/an
31	1531	98.8	308	7	ADN40061	Adn40061 Cancer/an
32	1531	98.8	308	8	ADP25261	Adp25261 PRO polyP
33	1506	97.2	289	8	ADR66910	Adr66910 Human pro
34	1506	97.2	289	8	ADR66012	Adr66012 Human pro
35	1464	94.5	283	8	ADJ87287	Adj87287 Human G p
36	893	57.6	203	2	AAW10664	Aaw10664 Human TGF
37	884.5	57.1	298	3	AAW79189	Aay79189 Haematopo
38	659	42.5	119	2	AAW31509	Aaw31509 Growth di
39	628	40.5	141	2	AAW10674	Aaw10674 TGF-beta-
40	626	40.4	154	2	AAW10665	Aaw10665 Human TGF
41	624	40.3	112	2	AAR84709	Aar84709 Human emb
42	624	40.3	112	4	AAW36558	Aaw36558 Human NOV
43	540	34.8	102	8	ADG71948	Adg71948 Human NOV
44	540	34.8	102	8	ADJ87285	Adj87285 Human G p
45	536	34.6	98	2	AAR77096	Aar77096 Human TGF

#### ALIGNMENTS

##### RESULT 1

AAAB36557

ID AAB36557 standard; protein; 295 AA.

XX AAB36557;

DT 07-MAR-2001 (first entry)

DE Human GDF-15 pre-pro-mature protein sequence.

XX Human; growth/differentiation factor; GDF; hGDF-15; neuroprotective;

KW transforming growth factor beta; TGF-beta; neurotrophic; diagnosis;  
KW neurodegenerative; detection; dopaminergic; cerebroprotective; stroke;  
KW antiParkinsonian; nootropic; neuroprotective; antidepressant; dementia;  
KW neuroleptic; neurodegenerative disorder; neurological disorder;  
KW psychological disorder; Parkinson's disease; Alzheimer's disease;  
KW central nervous system infection; psychiatric disorder; depression;  
KW schizophrenia; meningitis.

OS Homo sapiens.

XX WO200070051-A1.

XX 23-NOV-2000.

XX 16-MAY-2000; 2000WO-EP004445.

XX 17-MAY-1999; 99EP-00109714.

XX 29-JUL-1999; 99EP-00114853.

XX (BIOP-) BIOPHARM GDS BIOTECHNOLOGISCHEN ENTWICKL.

XX Unsicker K, Kriegelstein K;

XX WPI; 2001-016236/02;

XX N-PSDB; AAC88045.

XX Novel member of transforming growth factor-beta, GDF-15 which has  
neurotrophic effect on dopaminergic neurons, for treating  
neurodegenerative disorders such as Alzheimer's disease, Parkinson's  
disease and stroke.

XX Claim 10; Fig 7b; 37pp; English.

XX The present invention describes a transforming growth factor-beta (TGF-  
beta)-like protein designated growth/differentiation factor-15 (GDF-15)  
CC (1), which is derived from neurons and glial cells and which has a  
neurotrophic effect on dopaminergic (Daergic) neurons. (1) has

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:47:41 ; Search time 11.7545 Seconds  
(without alignments)  
711.279 Million cell updates/sec

Title: US-10-009-431-4  
Perfect score: 624  
Sequence: 1 ARNGDHCPGRCRLHTV.....DTGVSQTYDILLAKDCHCI 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp:\*\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp:\*\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp:\*\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp:\*\*
- 5: /cgn2\_6/ptodata/1/iaa/PCITUS COMB.pcp:\*\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	112	3	US-08-927-433-8
2	624	100.0	112	3	US-08-927-433-10
3	624	100.0	119	4	US-08-626-185-4
4	624	100.0	308	3	US-08-927-433-9
5	624	100.0	308	3	US-08-775-882-4
6	624	100.0	308	3	US-08-775-882-6
7	624	100.0	308	4	US-09-276-600-6
8	624	100.0	308	4	US-09-978-594-449
9	624	100.0	308	4	US-09-919-039-192
10	624	100.0	314	4	US-09-949-016-10118
11	620	99.4	295	2	US-08-411-607A-2
12	620	99.4	295	4	US-09-361-741-2
13	620	99.4	295	4	US-09-461-418-2
14	609	97.6	308	4	US-09-949-016-6559
15	545	87.3	99	3	US-08-775-882-2
16	456	73.1	115	4	US-09-463-931-2
17	201	32.2	36	4	US-09-276-600-7
18	196	31.4	117	4	US-09-374-958C-69
19	196	31.4	139	4	US-09-374-958C-68
20	195	31.2	118	1	US-08-481-377-14
21	195	31.2	118	3	US-08-491-835-12
22	195	31.2	118	3	US-09-153-733A-14
23	195	31.2	118	3	US-08-946-092A-12
24	195	31.2	118	3	US-09-172-062-12
25	195	31.2	118	3	US-09-301-520D-12
26	195	31.2	118	3	US-09-389-705-14
27	195	31.2	118	5	PCT-US94-006666-14

28	195	31.2	118	5	PCT-US94-00685-12	Sequence 12, Appl
29	195	31.2	438	2	US-08-459-346-14	Sequence 14, Appl
30	195	31.2	438	3	US-08-889-419-14	Sequence 14, Appl
31	195	31.2	438	3	US-08-402-542-14	Sequence 14, Appl
32	195	31.2	438	5	PCT-US93-07189-14	Sequence 14, Appl
33	195	31.2	455	1	US-08-278-729A-25	Sequence 25, Appl
34	195	31.2	455	1	US-08-155-343A-25	Sequence 25, Appl
35	195	31.2	455	1	US-08-406-672-25	Sequence 25, Appl
36	195	31.2	455	1	US-08-643-563A-25	Sequence 25, Appl
37	195	31.2	455	1	US-08-643-763A-25	Sequence 25, Appl
38	195	31.2	455	1	US-08-462-623-25	Sequence 25, Appl
39	195	31.2	455	1	US-08-451-953A-25	Sequence 25, Appl
40	195	31.2	455	2	US-08-459-346-16	Sequence 16, Appl
41	195	31.2	455	2	US-08-445-468A-25	Sequence 25, Appl
42	195	31.2	455	2	US-08-461-397A-25	Sequence 25, Appl
43	195	31.2	455	2	US-08-912-088-25	Sequence 25, Appl
44	195	31.2	455	3	US-08-278-730A-25	Sequence 25, Appl
45	195	31.2	455	3	US-08-889-419-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-927-433-8  
; Sequence 8, Application US/08927433  
; Patent No. 6107476  
; GENERAL INFORMATION:  
; APPLICANT: Erlander, Mark G.  
; APPLICANT: Huang, Shaoming  
; APPLICANT: Jackson, Michael A.  
; APPLICANT: Peterson, Per A.  
; TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND RELA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Johnson & Johnson  
; STREET: One J & J Plaza  
; CITY: New Brunswick  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08933  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/927,433  
; APPLICATION NUMBER: US/08/927,433  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Morrison, Alan J  
; REGISTRATION NUMBER: 37,399  
; REFERENCE/DOCKET NUMBER: ORT-849  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-524-3592  
; TELEFAX: 732-524-2808  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-927-433-8

Query Match 100.0%; Score 624; DB 3; Length 112;  
Best Local Similarity 100.0%; Pred. No. 3.3e-64;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ARNGDHCPGRCRLHTVRASLEDLGWADWVLSPREVQVTMCIGACPSQFRAANHAQ 60  
Db 1 ARNGDHCPGRCRLHTVRASLEDLGWADWVLSPREVQVTMCIGACPSQFRAANHAQ 60

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:49:12 ; Search time 32.3802 Seconds  
(without alignments)  
1245.908 Million cell updates/sec

Title: US-10-009-431-4  
Perfect score: 624  
Sequence: 1 ARNGDHCPLGRCRRLTV.....DTGVSLQTYDILLANDCHCI 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

```

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	119	15	US-10-373-581-4
2	624	100.0	283	15	US-10-211-689-76
3	624	100.0	308	9	US-09-276-600-6
4	624	100.0	308	9	US-09-981-353-188
5	624	100.0	308	10	US-09-919-039-192
6	624	100.0	308	13	US-10-000-628-6
7	624	100.0	308	15	US-10-257-597-2
8	624	100.0	308	16	US-10-425-115-229584
9	620	99.4	295	9	US-09-361-741-2
10	620	99.4	295	14	US-10-270-377-2
11	616	98.7	308	15	US-10-211-689-72
12	615	98.6	308	15	US-10-257-597-1
					Sequence 4, Appli
					Sequence 76, Appl
					Sequence 6, Appli
					Sequence 188, App
					Sequence 192, App
					Sequence 6, Appli
					Sequence 2, Appli
					Sequence 229584
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 72, Appl
					Sequence 1, Appli

```

609 97.6 308 14 US-10-205-823-327 Sequence 327, App
609 97.6 308 14 US-10-021-660-113 Sequence 113, App
609 97.6 308 15 US-10-295-027-618 Sequence 618, App
609 97.6 308 15 US-10-295-027-1379 Sequence 1379, App
609 97.6 308 15 US-10-211-462-191 Sequence 191, App
609 97.6 308 16 US-10-448-664-2 Sequence 2, Appli
609 86.5 102 15 US-10-211-689-74 Sequence 74, Appli
609 73.1 115 14 US-10-194-382-2 Sequence 68, Appli
609 69.1 298 9 US-09-789-919-68 Sequence 7, Appli
609 69.1 45 16 US-10-408-765A-976 Sequence 76, App
609 69.1 102 11 US-09-930-512-77 Sequence 77, Appli
609 69.1 102 15 US-10-080-334-210 Sequence 210, App
609 69.1 102 15 US-10-074-978A-300 Sequence 300, App
609 69.1 102 15 US-10-072-012-831 Sequence 831, App
609 69.1 102 15 US-10-072-012-833 Sequence 833, App
609 69.1 36 9 US-09-276-600-7 Sequence 7, Appli
609 69.1 36 13 US-10-000-628-7 Sequence 7, Appli
609 69.1 118 9 US-09-389-705-14 Sequence 14, Appli
609 69.1 118 13 US-10-115-406-12 Sequence 12, Appli
609 69.1 118 14 US-10-154-333-14 Sequence 14, Appli
609 69.1 118 16 US-10-704-223-12 Sequence 12, Appli
609 69.1 438 14 US-10-122-026-14 Sequence 14, Appli
609 69.1 455 8 US-08-260-675-25 Sequence 25, Appli
609 69.1 455 10 US-09-952-318A-25 Sequence 25, Appli
609 69.1 455 14 US-10-122-026-16 Sequence 16, Appli
609 69.1 455 14 US-10-050-050-25 Sequence 25, Appli
609 69.1 430 8 US-08-260-675-19 Sequence 19, Appli
609 69.1 430 16 US-10-385-064-16 Sequence 16, Appli
609 69.1 118 9 US-09-389-705-11 Sequence 11, Appli
609 69.1 118 14 US-10-154-333-11 Sequence 11, Appli
609 69.1 139 8 US-08-260-675-6 Sequence 6, Appli
609 69.1 139 10 US-09-952-318A-6 Sequence 6, Appli
609 69.1 139 14 US-10-050-050-6 Sequence 6, Appli

```

#### ALIGNMENTS

#### RESULT 1

```

US-10-373-581-4
; Sequence 4, Application US/10373581
; Publication No. US20030211541A1
; GENERAL INFORMATION:
; APPLICANT: Lee et al., Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-14
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/373,581
; FILING DATE: 24-Feb-2003
; CLASSIFICATION DATA:
; APPLICATION NUMBER: US/08/626,185
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:10 ; Search time 34.1545 Seconds  
(without alignments)  
1679.221 Million cell updates/sec

Title: US-10-009-431-4  
Perfect score: 624  
Sequence: 1 ARNGHCPGLGRCRLHTV.....DTGVSLQTYDILLAKDCHCI 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	308	1	GDFF HUMAN
2	624	100.0	308	2	Q9BWA0
3	456	73.1	303	1	GDFF MOUSE
4	456	73.1	303	2	Q6NX63
5	448	71.8	303	1	GDFF RAT
6	249	39.9	387	2	Q869H8
7	204	32.7	373	2	Q90723
8	204	32.7	373	2	Q98950
9	201	32.2	365	2	O02424
10	201	32.2	365	2	O76514
11	201	32.2	424	2	O6PAJ4
12	198	31.7	288	2	Q6PUB1
13	197.5	31.7	350	2	Q66KL4
14	197	31.6	441	2	O6PUD1
15	197	31.6	441	2	Q7P217
16	195	31.2	455	1	60A DROME
17	194.5	31.2	354	2	Q9YGV1
18	193	30.9	424	2	Q9YGH7
19	192	30.8	430	1	BMP7 MOUSE
20	191	30.6	436	1	60A DROVI
21	191	30.6	446	2	Q7T288
22	191	30.6	513	1	BMP5 HUMAN
23	190	30.4	426	1	BMP7 XENLA
24	190	30.4	426	2	O6PFF5
25	188	30.1	207	1	BMP6 RAT
26	188	30.1	313	2	Q91403
27	188	30.1	398	2	Q918T6
28	188	30.1	424	2	O6P2B8
29	188	30.1	431	1	BMP7 HUMAN
30	188	30.1	435	2	Q8BRW3
31	188	30.1	452	1	BMP5_MOUSE

32	188	30.1	453	2	P87373	P87373 gallus gall
33	188	30.1	454	1	BMP5_HUMAN	P22003 homo sapien
34	188	30.1	454	2	Q8CCE0	Q8CCE0 mus musculus
35	188	30.1	506	2	Q811S4	Q811S4 rattus norv
36	188	30.1	510	1	BMP6_MOUSE	P20722 mus musculus
37	187	30.0	355	1	DVR1_BRARE	P35621 brachydanio
38	185	29.6	356	2	Q7T2G5	Q7T2G5 xenopus lae
39	185	29.6	360	1	DVR1_XENLA	P09534 xenopus lae
40	184	29.5	432	2	Q9PTF9	Q9PTF9 brachydanio
41	182	29.2	444	2	Q6GUA6	Q6GUA6 sus scrofa
42	182	29.2	453	1	GDF9_CAPHI	Q66nc0 capra hircu
43	182	29.2	453	1	GDF9_SHEEP	Q77681 ovis aries
44	181	29.0	444	2	Q6DOX1	Q6dql1 sus scrofa
45	180.5	28.9	382	2	Q8HY13	Q8hy13 trichosurus

#### ALIGNMENTS

RESULT 1  
ID GDFF\_HUMAN STANDARD; PRT; 308 AA.  
AC Q99988; O14629; P78360; Q9NRT0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 44, Last sequence update)  
DE Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1).  
DE Name=GDF15; Synonyms=MIC1, PDF, PLAB, PTGFB;  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibrosarcoma;  
RX MEDLINE=98006316; PubMed=9348093;  
RA Yokoyama-Kobayashi M., Saeki M., Sekine S., Kato S.;  
RT "Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in placenta."  
RL J. Biochem. 122:622-626(1997).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=97470998; PubMed=9326641; DOI=10.1073/pnas.94.21.11514;  
RX Bootcov M.R., Bauakin A.R., Valenzuela S.M., Moore A.G., Bansal M., He X.Y., Zhang H.P., Donnellan M., Mahler S., Pryor K., Walsh B.J., Nicholson R.C., Fairlie W.D., For S.B., Robbins J.M., Breit S.N.;  
RA "MIC-1, a novel macrophage inhibitory cytokine, is a divergent member of the TGF-beta superfamily."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:11514-11519(1997).  
[3]  
SEQUENCE FROM N.A.  
TISSUE=Placenta;  
RX MEDLINE=98041637; PubMed=9375789; DOI=10.1016/S0167-4781(97)00122-X;  
RA Hromas R., Hufford M., Sutton J., Xu D., Li Y., Lu L.;  
RT "PLAB, a novel placental bone morphogenetic protein."  
RL Biochim. Biophys. Acta 1354:40-44(1997).  
[4]  
SEQUENCE FROM N.A.  
TISSUE=Placenta;  
RX MEDLINE=98256302; PubMed=9593718; DOI=10.1074/jbc.273.22.13760;  
RA Paralkar V.M., Vail A.L., Grasser W.A., Brown T.A., Xu H., Vukicevic S., Ke H.Z., Qi H., Owen T.A., Thompson D.D.;  
RT "Cloning and characterization of a novel member of the transforming growth factor-beta/bone morphogenetic protein family."  
RL J. Biol. Chem. 273:13760-13767(1998).  
[5]  
SEQUENCE OF 14-308 FROM N.A.  
MEDLINE=98085971; PubMed=9426002; DOI=10.1016/S0378-1119(97)00485-X;  
RA Lawton L.N., de Fatima Bonaldo M., Jelenc P.C., Qiu L., Baumes S.A., Marcelino R.A., de Jesus G.M., Wellington S., Knowles J.A.,



Best Local Similarity 36.3%;

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:29:15 ; Search time 72 Seconds  
(without alignments)  
601.627 Million cell updates/sec

Title: US-10-009-431-4

Perfect score: 624

Sequence: 1. ARNGDHCPGRCRLHTV.....DTGVSQTYDILLAKDCHCI 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	112	2	AAR84709 Human emb
2	624	100.0	112	2	AAB36558 Human GDP
3	624	100.0	119	2	AAB31509 Growth di
4	624	100.0	141	2	AAW10674 TGF-beta-
5	624	100.0	154	2	AAW10665 Human TGF
6	624	100.0	203	2	AAW10664 Human TGF
7	624	100.0	283	8	ADJ87287 Human G p
8	624	100.0	295	4	AAB36557 Human GDP
9	624	100.0	308	2	AAR77097 Human TGF
10	624	100.0	308	2	AAR84710 Human emb
11	624	100.0	308	2	AAW10673 Human TGF
12	624	100.0	308	2	AAW10666 Human TGF
13	624	100.0	308	2	AAW10672 Human TGF
14	624	100.0	308	2	AAW10662 Human TGF
15	624	100.0	308	2	AAW10668 Human TGF
16	624	100.0	308	2	AAW10667 Human TGF
17	624	100.0	308	2	AAW10671 Human TGF
18	624	100.0	308	2	AAW48672 GP-2H pro
19	624	100.0	308	3	AAB26122 Human TGF
20	624	100.0	308	5	ABB09174 Human NAG
21	624	100.0	308	5	AAE13538 Human mac
22	624	100.0	308	6	ADA11070 Human cdn
23	624	100.0	308	7	ADI63071 Human apo
24	624	100.0	308	8	ADE77027 Human pro
25	624	100.0	308	8	ADL12720 Human ste

26	624	100.0	308	8	ABM82070	Abm82070 Tumour-as
27	624	100.0	318	2	AAW10663	AAW10663 Human TGF
28	620	99.4	295	2	AAW02613	AAW02613 Human pro
29	616	98.7	308	8	ADG71946	ADG71946 Human NOV
30	616	98.7	308	8	ADJ87283	ADJ87283 Human G p
31	615	98.6	308	2	AAW10670	AAW10670 Human TGF
32	615	98.6	308	2	AAW10669	AAW10669 Human TGF
33	615	98.6	308	5	AAE13539	AAE13539 Human mac
34	609	97.6	289	8	ADR66910	ADR66910 Human pro
35	609	97.6	289	8	ADR66012	ADR66012 Human pro
36	609	97.6	308	6	ABU03550	ABU03550 Angiogene
37	609	97.6	308	6	ABU56743	ABU56743 Lung canc
38	609	97.6	308	7	ADB75503	ADB75503 Prostate
39	609	97.6	308	7	ADN39300	ADN39300 Cancer/an
40	609	97.6	308	7	ADN40061	ADN40061 Cancer/an
41	609	97.6	308	8	ADP25261	ADP25261 PRO polyp
42	540	86.5	102	8	ADG71948	ADG71948 Human NOV
43	540	86.5	102	8	ADJ87285	ADJ87285 Human G p
44	536	85.9	98	2	AAR77096	AAR77096 Human TGF
45	456	73.1	115	2	AAW93161	AAW93161 Murine GD

#### ALIGNMENTS

##### RESULT 1

AAR84709

ID AAR84709 standard; protein; 112 AA.

XX AAR84709;

XX 23-MAY-1996 (first entry)

XX Human embryonal lung mature protein.

XX Eosinophil; inhibitor; active oxygen production; bronchial asthma; human;

XX embryonal lung.

XX Homo sapiens.

XX JF07258293-A.

XX 09-OCT-1995.

XX 23-MAR-1994; 94JP-00052225.

XX 23-MAR-1994; 94JP-00052225.

XX (ASAH ) ASAH KASEI KOGYO KK.

XX WPI; 1995-380074/49.

XX N-PSDB; AAT05177.

XX A new protein for the treatment of bronchial asthma - inhibits the production of active oxygen in eosinophil(s).

XX Claim 1; Page 2; 26pp; Japanese.

XX The present sequence is that of a 112 amino acid mature protein isolated from normal diploid cells of human embryonal lung tissue. The protein inhibits production of active oxygen in eosinophils and is useful for treatment and prevention of bronchial asthma

XX Sequence 112 AA;

Query Match 100.0%; Score 624; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 48-57;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNGDHCPGRCRLHTVTRASLEDLGNADWVLSPREVQVTMCIGACPSQFRAANHAQ 60

DB 1 ARNGDHCPGRCRLHTVTRASLEDLGNADWVLSPREVQVTMCIGACPSQFRAANHAQ 60

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:47:41 ; Search time 10.2851 Seconds  
(without alignments)  
711.279 Million cell updates/sec

Title: US-10-009-431-4\_COPY\_14\_111  
Perfect score: 541  
Sequence: 1 CCRHTVTRASLEGLGWADWV.....TDTGVSLSQTYDDLLKNDCHC 98

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	100.0	99	3	US-08-775-882-2
2	541	100.0	112	3	US-08-927-433-8
3	541	100.0	112	3	US-08-927-433-10
4	541	100.0	119	4	US-08-626-185-4
5	541	100.0	308	3	US-08-927-433-9
6	541	100.0	308	3	US-08-775-882-4
7	541	100.0	308	3	US-08-775-882-6
8	541	100.0	308	4	US-08-276-600-6
9	541	100.0	308	4	US-08-976-594-449
10	541	100.0	308	4	US-08-919-039-192
11	541	100.0	314	4	US-08-949-016-10118
12	537	99.3	295	2	US-08-411-607A-2
13	537	99.3	295	4	US-08-361-741-2
14	537	99.3	295	4	US-08-461-418-2
15	535	98.9	308	4	US-08-949-016-6559
16	407	75.2	115	4	US-08-463-931-2
17	195	36.0	117	4	US-08-374-958C-69
18	195	36.0	139	4	US-08-374-958C-68
19	195	36.0	438	2	US-08-459-346-14
20	195	36.0	438	3	US-08-889-419-14
21	195	36.0	438	3	US-08-402-542-14
22	195	36.0	438	5	PCT-US93-07189-14
23	193	35.7	102	4	US-08-374-958C-53
24	193	35.7	430	1	US-07-841-646-25
25	193	35.7	430	1	US-07-901-703-9
26	193	35.7	430	3	US-08-445-467-19
27	193	35.7	430	4	US-08-464-206-16

28	193	35.7	430	4	US-08-404-113A-16
29	193	35.7	430	4	US-08-260-675-19
30	193	35.7	430	5	PCT-US90-07654-2
31	193	35.7	430	5	PCT-US92-01968-19
32	193	35.7	430	5	PCT-US93-05446-9
33	193	35.7	430	5	PCT-US93-07190-19
34	193	35.7	430	5	PCT-US93-07231-19
35	193	35.7	430	5	PCT-US93-08742-19
36	193	35.7	430	5	PCT-US93-08808-19
37	193	35.7	430	5	PCT-US93-08885-19
38	193	35.7	430	5	PCT-US93-10520-6
39	192	35.5	118	1	US-08-481-377-11
40	192	35.5	118	3	US-09-153-733A-11
41	192	35.5	118	3	US-09-389-705-11
42	192	35.5	118	5	PCT-US94-00666-11
43	191	35.3	102	2	US-08-288-508C-17
44	191	35.3	102	3	US-08-478-097A-14
45	191	35.3	102	3	US-08-289-222E-26

# ALIGNMENTS

RESULT 1  
US-08-775-882-2  
; Sequence 2, Application US/08775882  
; Patent No. 6180602  
; GENERAL INFORMATION:  
; APPLICANT: KATO, Seishi  
; APPLICANT: OH, Suwan  
; APPLICANT: SEKINE, Shingo  
; APPLICANT: SAKI, Minoru  
; APPLICANT: KOBAYASHI, Midori  
; APPLICANT: YADA, Mika  
; APPLICANT: TSUJI, Tomoko  
; APPLICANT: OHMORI, Hitoshi  
; TITLE OF INVENTION: HUMAN NOVEL CDNA, TGF-BETA SUPERFAMILY  
; TITLE OF INVENTION: PROTEIN ENCODED THEREBY AND THE USE AS IMMUNOSUPPRESSIVE  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/775,882  
; FILING DATE: 02-JAN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/390,207  
; FILING DATE: 16-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/379,441  
; FILING DATE: 03-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-61431  
; FILING DATE: 26-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-327619  
; FILING DATE: 13-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-208077  
; FILING DATE: 04-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:49:12 ; Search time 28.3327 Seconds  
(without alignments)  
1245.908 Million cell updates/sec

Title: US-10-009-431-4\_COPY\_14\_111

Perfect score: 541

Sequence: 1 CCELTHTVRASLEGLGWADWV.....TTGVSQTYDILLAKDCHC 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA.\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pcp.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pcp.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pcp.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pcp.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pcp.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pcp.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pcp.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pcp.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pcp.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pcp.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pcp.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pcp.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pcp.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pcp.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	119	15	US-10-373-581-4
2	541	100.0	283	15	US-10-211-689-76
3	541	100.0	308	9	US-09-276-600-6
4	541	100.0	308	9	US-09-981-353-188
5	541	100.0	308	10	US-09-919-039-192
6	541	100.0	308	13	US-10-000-628-6
7	541	100.0	308	15	US-10-257-597-1
8	541	100.0	308	15	US-10-257-597-2
9	541	100.0	308	16	US-10-425-115-229584
10	537	99.3	295	9	US-09-361-741-2
11	537	99.3	295	14	US-10-270-377-2
12	535	98.9	308	14	US-10-205-823-327

13	535	98.9	308	14	US-10-021-660-113	Sequence 113, App
14	535	98.9	308	15	US-10-295-027-618	Sequence 618, App
15	535	98.9	308	15	US-10-295-027-1379	Sequence 1379, App
16	535	98.9	308	15	US-10-211-462-191	Sequence 191, App
17	535	98.9	308	16	US-10-448-664-2	Sequence 2, Appli
18	533	98.5	308	15	US-10-211-689-72	Sequence 72, Appli
19	532	98.3	308	15	US-10-211-689-74	Sequence 74, Appli
20	407	75.2	115	14	US-10-194-382-2	Sequence 2, Appli
21	382	70.6	298	9	US-09-789-919-68	Sequence 68, Appli
22	240	44.4	45	16	US-10-408-765A-976	Sequence 976, App
23	205	37.9	102	11	US-09-930-512-77	Sequence 77, Appli
24	205	37.9	102	15	US-10-080-334-210	Sequence 210, App
25	205	37.9	102	15	US-10-074-978A-300	Sequence 300, App
26	205	37.9	102	15	US-10-072-012-831	Sequence 831, App
27	205	37.9	102	15	US-10-072-012-833	Sequence 833, App
28	195	36.0	438	14	US-10-122-026-14	Sequence 14, Appli
29	193	35.7	430	8	US-08-260-675-19	Sequence 19, Appli
30	193	35.7	430	16	US-10-385-064-16	Sequence 16, Appli
31	192	35.5	118	9	US-09-389-705-11	Sequence 11, Appli
32	192	35.5	118	14	US-10-154-333-11	Sequence 11, Appli
33	191	35.3	102	10	US-09-952-318A-28	Sequence 28, Appli
34	191	35.3	102	14	US-10-187-394-14	Sequence 14, Appli
35	191	35.3	118	13	US-10-115-406-9	Sequence 9, Appli
36	191	35.3	118	16	US-10-704-223-9	Sequence 9, Appli
37	191	35.3	139	8	US-08-260-675-6	Sequence 6, Appli
38	191	35.3	139	10	US-09-952-318A-6	Sequence 6, Appli
39	191	35.3	139	14	US-10-050-050-6	Sequence 6, Appli
40	191	35.3	139	15	US-10-366-345-62	Sequence 62, Appli
41	191	35.3	139	16	US-10-385-064-6	Sequence 6, Appli
42	191	35.3	143	13	US-10-002-278-5	Sequence 5, Appli
43	191	35.3	430	8	US-08-957-425-25	Sequence 25, Appli
44	191	35.3	430	10	US-09-952-318A-19	Sequence 19, Appli
45	191	35.3	430	14	US-10-122-026-4	Sequence 4, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-373-581-4  
; Sequence 4, Application US/10373581  
; Publication No. US20030211541A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee et al., Se-Jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-14  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/373,581  
; FILING DATE: 24-Feb-2003  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/626,185  
; FILING DATE: 29-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 4:

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:10 ; Search time 29.8851 Seconds  
(without alignments)  
1679.221 Million cell updates/sec

Title: US-10-009-431-4\_COPY\_14\_111

Perfect score: 541

Sequence: 1 CRLHTVRASLEDLGWADWV.....TDGTGVSLOTYYDLLAKDCHC 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	541	100.0	308	1	GDFF_HUMAN	Q99888 homo sapien
2	541	100.0	308	2	Q9BWA0	Q9BWA0 homo sapien
3	407	75.2	303	1	GDFF_MOUSE	Q92017 mus musculus
4	407	75.2	303	2	G6NXG3	G6NXG3 mus musculus
5	399	73.8	303	1	GDFF_RAT	Q92016 rattus norv
6	239	44.2	387	2	Q869H8	Q869H8 crassostrea
7	201	37.2	365	2	O02424	O02424 caenorhabdi
8	201	37.2	365	2	O76514	O76514 caenorhabdi
9	200	37.0	424	2	G6P4J4	G6P4J4 xenopus tro
10	195	36.0	288	2	G6PUB1	G6PUB1 anopheles s
11	194	35.9	441	2	G6PUD1	G6PUD1 anopheles s
12	194	35.9	441	2	Q7PZ17	Q7PZ17 anopheles g
13	192	35.5	424	2	Q9YGH7	Q9YGH7 xenopus lae
14	191	35.3	430	1	BMP7_MOUSE	P23359 mus musculus
15	191	35.3	513	1	BMP6_HUMAN	P22004 homo sapien
16	189	34.9	373	2	Q90723	Q90723 gallus gall
17	189	34.9	373	2	Q98950	Q98950 gallus gall
18	188	34.8	207	1	BMP6_RAT	Q04906 rattus norv
19	188	34.8	350	2	G66KL4	G66KL4 xenopus tro
20	188	34.8	426	1	BMP7_XENLA	Q66KL4 xenopus lae
21	188	34.8	426	2	G6PF75	G6PF75 xenopus lae
22	188	34.8	435	2	Q8BRW3	Q8BRW3 mus musculus
23	188	34.8	506	2	G811S4	Q811S4 rattus norv
24	188	34.8	510	1	BMP6_MOUSE	P20722 mus musculus
25	187	34.6	313	2	Q91403	Q91403 gallus gall
26	187	34.6	398	2	Q918T6	Q918T6 gallus gall
27	187	34.6	424	2	G6F2B8	G6F2B8 xenopus tro
28	187	34.6	431	1	BMP7_HUMAN	P18075 homo sapien
29	187	34.6	436	1	60A_DROVI	Q24735 drosophila
30	187	34.6	455	1	60A_DROME	P27091 drosophila
31	186	34.4	446	2	Q7T288	Q7T288 brachydanio

32 185 34.2 354 2 Q9YGV1 Q9YGV1 xenopus lae  
33 184 34.0 452 1 BMP5\_MOUSE BMP5\_MOUSE mus musculus  
34 184 34.0 453 2 P87373 P87373 gallus gall  
35 184 34.0 454 1 BMP5\_HUMAN BMP5\_HUMAN mus musculus  
36 184 34.0 454 2 Q8CCE0 Q8CCE0 mus musculus  
37 181 33.5 356 2 Q7T2G5 Q7T2G5 xenopus bor  
38 181 33.5 360 1 DVRL\_XENLA DVRL\_XENLA xenopus lae  
39 180 33.3 382 2 Q8HYI3 Q8HYI3 trichosurus  
40 180 33.3 432 2 Q9PTF9 Q9PTF9 brachydanio  
41 180 33.3 444 2 Q6DQX1 Q6DQX1 sus scrofa  
42 180 33.3 444 2 Q6GUA6 Q6GUA6 sus scrofa  
43 180 33.3 453 1 GDF9\_CAPHI GDF9\_CAPHI capra hircu  
44 180 33.3 453 1 GDF9\_SHEEP GDF9\_SHEEP ovis aries  
45 178 32.9 453 2 Q9GK68 Q9GK68 bos taurus

#### ALIGNMENTS

RESULT 1  
ID GDFF\_HUMAN STANDARD; PRT; 308 AA.  
AC Q99888; O14629; P78360; Q9NRTO; Q9NRTO;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 03-JUL-2004 (Rel. 44, Last annotation update)  
DE Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory DE cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated DE protein 1) (NRG-1)  
DE Names=GDF15; Synonyms=MIC1, PDF, PLAB, PTGFB;  
GN Homo sapiens (Human)  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Fibrosarcoma;  
RC MEDLINE=98006316; PubMed=9348093;  
RX Yokoyama-Kobayashi M., Saeki M., Sekine S., Kato S.;  
RA "Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in placenta";  
RT J. Biochem. 122:622-626(1997).  
[2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=97470998; PubMed=9326641; DOI=10.1073/pnas.94.21.11514;  
RX Bootcov M.R., Bauekin A.R., Valenzuela S.M., Moore A.G., Bansal M., He X.Y., Zhang H.P., Domellian M., Mahler S., Pryor K., Walsh B.J., Nicholson R.C., Fairlie W.D., Por S.B., Robbins J.M., Breit S.N.;  
RA "MIC-1, a novel macrophage inhibitory cytokine, is a divergent member of the TGF-beta superfamily";  
RT Proc. Natl. Acad. Sci. U.S.A. 94:11514-11519(1997).  
[3]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Placenta;  
RC MEDLINE=98041637; PubMed=9375789; DOI=10.1016/S0167-4781(97)00122-X;  
RX Thomas R., Hufford M., Sutton J., Xu D., Li Y., Lu L.;  
RA "PLAB, a novel placental bone morphogenetic protein";  
RT Biochim. Biophys. Acta 1354:40-44(1997).  
[4]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Placenta;  
RC MEDLINE=98256302; PubMed=9593718; DOI=10.1074/jbc.273.22.13760;  
RX Paralkar V.M., Vail A.L., Grasser W.A., Brown T.A., Xu H., Vukicevic S., Ke H.Z., Qi H., Owen T.A., Thompson D.D.;  
RT "Cloning and characterization of a novel member of the transforming growth factor-beta/bone morphogenetic protein family";  
RT J. Biol. Chem. 273:13760-13767(1998).  
[5]  
RN SEQUENCE OF 14-308 FROM N.A.  
RP MEDLINE=98085971; PubMed=9426002; DOI=10.1016/S0378-1119(97)00485-X;  
RX Lawton L.N., de Fatima Bonaudo M., Jelenc P.C., Qiu L., Baumes S.A., Marcelino R.A., de Jesus G.M., Wellington S., Knowles J.A.,

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:46 ; Search time 8.53861 Seconds  
(without alignments)  
1104.306 Million cell updates/sec

Title: US-10-009-431-4\_COPY\_14\_111  
Perfect score: 541  
Sequence: 1 CCRLLHTVRASLEDLGWADWV.....TDTGVSLOTQYDILLAKDCHC 98

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	100.0	309	2 JC5697	placental transfor
2	201	37.2	365	2 T43286	cet-1 protein - Ca
3	191	35.3	430	2 J01184	osteogenic protein
4	191	35.3	513	1 BMH06	bone morphogenetic
5	188	34.8	207	2 S37618	vgr protein - rat
6	188	34.8	426	2 JH0690	bone morphogenetic
7	188	34.8	510	2 A54798	Vg-1-related prote
8	187	34.6	313	2 I51284	bone morphogenetic
9	187	34.6	431	1 BMH07	bone morphogenetic
10	187	34.6	455	2 A43918	TGF-beta-related p
11	184	34.0	452	2 T49542	bone morphogenetic
12	184	34.0	454	1 BMH05	bone morphogenetic
13	181	33.5	360	2 A29619	Vgl embryonic grow
14	173	32.0	151	2 S43296	bone morphogenetic
15	173	32.0	402	2 A45056	osteogenic protein
16	172	31.8	441	2 S45284	growth/differentia
17	170	31.4	588	2 A26158	decapentaplegic pr
18	168	31.1	495	2 S43294	bone morphogenetic
19	168	31.1	501	2 JC2347	growth/differentia
20	168	31.1	501	2 A55452	cartilage-derived
21	164.5	30.4	354	2 S29718	gene nodal protein
22	163	30.1	461	2 S2408	SPVRI protein - s
23	161	29.8	125	2 S43295	bone morphogenetic
24	160.5	29.7	366	2 A46607	growth/differentia
25	159	29.4	372	2 C39364	GDP-1 embryonic gr
26	156	28.8	436	2 B55452	cartilage-derived
27	155.5	28.7	366	2 A45402	transforming growt
28	152.5	28.2	357	2 A39364	GDP-1 embryonic gr
29	150.5	27.8	350	2 JC5241	activin beta E cha

30	147.5	27.3	401	2 JH0689	bone morphogenetic
31	147.5	27.3	408	1 BMH04	bone morphogenetic
32	147.5	27.3	408	2 S58791	bone morphogenetic
33	147.5	27.3	408	2 S38343	bone morphogenetic
34	147.5	27.3	420	2 T49541	bone morphogenetic
35	147.5	27.3	427	2 A40735	TGF beta homolog d
36	146.5	27.1	400	2 A49147	bone morphogenetic
37	146.5	27.1	405	2 T50608	bone morphogenetic
38	146.5	27.1	476	2 JC4646	bone morphogenetic
39	144.5	26.7	472	1 BMH03	bone morphogenetic
40	143.5	26.5	360	2 T53032	bone morphogenetic
41	143.5	26.5	398	2 JH0688	bone morphogenetic
42	143.5	26.5	398	2 JH0687	bone morphogenetic
43	143.5	26.5	478	2 JC4838	bone morphogenetic
44	141	26.1	365	2 T03907	TGF-beta-related p
45	140.5	26.0	408	2 JH0801	bone morphogenetic

ALIGNMENTS

RESULT 1

JC5697

Placental transforming growth factor-beta homolog - human  
C:Species: Homo sapiens (man)

C:Date: 20-Nov-1997 #sequence\_revision 20-Nov-1997 #text\_change 09-Jul-2004

C:Accession: JC5697

R:Yokoyama-Kobayashi, M.; Saeki, M.; Sekine, S.; Kato, S.

J. Biochem. 122, 622-626, 1997

A:Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in

A:Reference number: JC5697; MUID:98006316; PMID:9348093

A:Accession: JC5697

A:Molecule type: mRNA

A:Residues: 1-309 <YOK>

A:Cross-references: UNIPROT:Q9BWA0; DDBJ:AB0000584

A:Experimental source: fibrosarcoma

C:Comment: This protein plays a role in reproduction.

Query Match 100.0%; Score 541; DB 2; Length 309;

Best Local Similarity 100.0%; Pred. No. 5.8e-51;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCRLLHTVRASLEDLGWADWVLSPREVQVTWCIGACPSQFRAANVHAQIKTSLHRLKPDV 60

Db 211 CCRLLHTVRASLEDLGWADWVLSPREVQVTWCIGACPSQFRAANVHAQIKTSLHRLKPDV 270

Qy 61 PAPCCVPASYNPMVLIOKTDGTGVSLOTQYDILLAKDCHC 98

Db 271 PAPCCVPASYNPMVLIOKTDGTGVSLOTQYDILLAKDCHC 308

RESULT 2

T43286

cet-1 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C:Accession: T43286

R:Morita, K.; Chow, K.L.; Ueno, N.

Development 126, 1337-1347, 1999

A:Title: Regulation of body length and male tail ray pattern formation of Caenorhabditis

A:Reference number: 222393; MUID:99146896; PMID:10021351

A:Accession: T43286

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-365 <MOR>

A:Cross-references: UNIPROT:O76514; EMBL:AF074395; NID:G3328181; PIDN:AAC36791.1; PID:9

C:Genetics:

A:Gene: cet-1

A:Map position: 5

C:Superfamily: inhibin

Query Match 37.2%; Score 201; DB 2; Length 365;

Best Local Similarity 36.3%; Pred. No. 4.3e-14;

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:29:15 ; Search time 63 Seconds  
(without alignments)

601.627 Million cell updates/sec

Title: US-10-009-431-4\_COPY\_14\_111

Perfect score: 541

Sequence: 1 CCRLLHTVRASLEDLGWADWV.....TDTGVSLQTYDILLAKDCHC 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	541	100.0	112	2	AAR84709	Human emb
2	541	100.0	112	4	AAB36558	Human GDF
3	541	100.0	119	2	AAW31509	Growth di
4	541	100.0	141	2	AAW10674	TGF-beta-
5	541	100.0	154	2	AAW10665	Human TGF
6	541	100.0	203	2	AAW10664	Human TGF
7	541	100.0	283	8	ADJ87287	Human G p
8	541	100.0	295	4	AAB36557	Human GDF
9	541	100.0	308	2	AAR77097	Human TGF
10	541	100.0	308	2	AAR84710	Human emb
11	541	100.0	308	2	AAW10673	Human TGF
12	541	100.0	308	2	AAW10666	Human TGF
13	541	100.0	308	2	AAW10670	Human TGF
14	541	100.0	308	2	AAW10672	Human TGF
15	541	100.0	308	2	AAW10669	Human TGF
16	541	100.0	308	2	AAW10662	Human TGF
17	541	100.0	308	2	AAW10668	Human TGF
18	541	100.0	308	2	AAW10667	Human TGF
19	541	100.0	308	2	AAW10671	Human TGF
20	541	100.0	308	2	AAW48672	GF-2H pro
21	541	100.0	308	3	AAB26122	Human TGF
22	541	100.0	308	5	ABE09174	Human NAG
23	541	100.0	308	5	AAE13538	Human mac
24	541	100.0	308	5	AAE13539	Human mac
25	541	100.0	308	6	ADA11070	Human cDN

## ALIGNMENTS

### RESULT 1

AAR84709  
ID AAR84709 standard; protein; 112 AA.

AC AAR84709;

DT 23-MAY-1996 (first entry)

DE Human embryonal lung mature protein.

XX Eosinophil; inhibitor; active oxygen production; bronchial asthma; human;  
KW embryonal lung.

OS Homo sapiens.

PN JP07258293-A.

XX 09-OCT-1995.

PF 23-MAR-1994; 94JP-00052225.

PR 23-MAR-1994; 94JP-00052225.

XX (ASAH ) ASAH KASEI KOGYO KK.

XX WPI; 1995-380074/49.

DR N-PSDB; AAT05177.

XX A new protein for the treatment of bronchial asthma - inhibits the  
PT production of active oxygen in eosinophil(s).

PS Claim 1; Page 2; 26pp; Japanese.

CC The present sequence is that of a 112 amino acid mature protein isolated  
CC from normal diploid cells of human embryonal lung tissue. The protein  
CC inhibits production of active oxygen in eosinophils and is useful for  
CC treatment and prevention of bronchial asthma

SQ Sequence 112 AA;

Query Match 100.0%; Score 541; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 1.3e-51;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCRLLHTVRASLEDLGWADWVLSPREVQVTWCIGACPSQFRAANHHQAQIKTSLHRLKPDV 60

Db 14 CCRLLHTVRASLEDLGWADWVLSPREVQVTWCIGACPSQFRAANHHQAQIKTSLHRLKPDV 73

Adi63071 Human apo  
Ad577027 Human pro  
Adl12720 Human ste  
Abm82070 Tumour-as  
Aw10563 Human TGF  
Aaw02613 Human pro  
Adr66910 Human pro  
Adr66012 Human pro  
Abu03550 Angiogene  
Abu56743 Lung can  
Adb75503 Prostate  
Adn39300 Cancer/an  
Adm40061 Cancer/an  
Adp25261 PRO poly  
Adg71946 Human NOV  
Adj87283 Human G p  
Aar77096 Human TGF  
Adg71948 Human NOV  
Adj87285 Human G p  
Aaw93161 Murine GD

26 541 100.0 308 7 ADI63071  
27 541 100.0 308 8 ADE77027  
28 541 100.0 308 8 ADL12720  
29 541 100.0 308 8 ABM82070  
30 541 100.0 318 2 AAW10563  
31 537 99.3 295 2 AAW02613  
32 535 98.9 289 8 ADR66910  
33 535 98.9 289 8 ADR66012  
34 535 98.9 308 6 ABU03550  
35 535 98.9 308 6 ABU56743  
36 535 98.9 308 7 ADB75503  
37 535 98.9 308 7 ADN39300  
38 535 98.9 308 7 ADN40061  
39 535 98.9 308 8 ADP25261  
40 533 98.5 308 8 ADG71946  
41 533 98.5 308 8 ADJ87283  
42 532 98.3 98 2 AAR77096  
43 532 98.3 102 8 ADG71948  
44 532 98.3 102 8 ADJ87285  
45 407 75.2 115 2 AAW93161